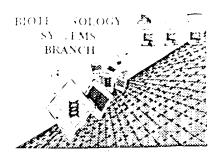
RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	111111
Source:	1, 2, 5
Date Processed by STIC:	

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

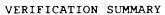
Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

PCT09

DATE: 10/30/2001

PATENT APPLICATION: US/09/856,543 TIME: 13:16:02 Input Set : A:\01632002.app Combined Diskette Needed 3 <110 · APPLICANT: Hartwich, Gerhard 4 Heller, Adam $6\!<\!120$ - TITLE OF INVENTION: METHOD FOR THE ELECTROCHEMICAL DETECTION OF NUCLEIC 7 ACID OLIGOMER HYBRIDS 9 <130 > FILE REFERENCE: 0163-2002 11 <140 > CURRENT APPLICATION NUMBER: 09/856,543 12 < 141 - CURRENT FILING DATE: 1999-11-19 14 -: 150> PRIOR APPLICATION NUMBER: PCT/EP99/08888 15 <151> PEIOR FILING DATE: 1998-11-23 17 <160 NUMBER OF SEQ ID NOS: 2 19 <170> SOFTWARE: PatentIn Ver. 2.0 21 < 210 > SEQ ID NO: 122 <2115 LENGTH: 12 23 <212> TYPE: PRT 24 <213> OFGANISM: Unknown F-26 <220> FEATURE: Item 11 W-->(28 < 223> OTHER INFORMATION:28 4005 SEQUENCE: 1 24 Thr Ala Gly Thr Cys Gly Gly Ala Ala Gly Cys Ala 30 1 5 33 <210> SEQ ID NO: 2 34 <211> LENGTH: 12 35 <212> TYPE: PRT 36 <213> ORGANISM: Unknown 38 <220 FEATURE: W-- 2 40 <223 > OTHER INFORMATION: 40 <400> SEQUENCE: 2 41 Ala Thr Cys Ala Gly Ala Thr Thr Thr Cys Gly Thr 42 1

RAW SEQUENCE LISTING



PATENT APPLICATION: US/09/856,543 TIME: 13:16:03

DATE: 10/30/2001

Input Set : A:\01632002.app

Output Set: N:\CRF3\10302001\I856543.raw

L:28 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: L:40 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

Raw Sequence Listing Error Summary

SERIAL NUMBER: 01/856543 SUGGESTED CORRECTION ERROR DETECTED ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping" Invalid Line Length. The rules require that a line not exceed 72 characters in length. This includes white spaces. The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; Misaligned Amino Numbering use space characters, instead. The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please Non-ASCII ensure your subsequent submission is saved in ASCII text. Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, Variable Length each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid PatentIn 2.0 Normally, PatentIn would automatically generate this section from the "bug" previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (OLD RULES) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. missing. If intentional, please insert the following lines for each skipped sequence. Skipped Sequences Sequence(s) (NEW RULES) <210> sequence id number <400> sequence id number 000 Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of n's or Xaa's Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. (NEW RULES) In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence Sequence(s) 1+2 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, PatentIn 2.0 resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence "bug" listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk